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protocols2-nj.html July, 1998). STCs can represent a copy of up to a full length of a mRNA transcript, a promoter element or part of a promoter, can contain simple sequence repeats (also called microsatellites) repetitive elements or fragments of repetitive elements, other DNA markers, or any combination thereof.

Please **delete** the paragraph at page 5, lines 6 through 15 and **replace** it with the following paragraph:

B2

Similarity analysis includes database search and alignment. Examples of public databases include the DNA Database of Japan (DDBJ) (www-ddbj.nig.ac.jp/); Genebank (www-ncbi.nlm.nih.gov/web/Genbank/Index.html); and the European Molecular Biology Laboratory Nucleic Acid Sequence Database (EMBL) (www-ebi.ac.uk/ebi_docs/embl_db.html). A number of different search algorithms have been developed, one example of which are the suite of programs referred to as BLAST programs. There are five implementations of BLAST, three designed for nucleotide sequences queries (BLASTN, BLASTX, and TBLASTX) and two designed for protein sequence queries (BLASTP and TBLASTN) (Coulson, *Trends in Biotechnology*, 12:76-80 (1994); Birren, *et al.*, *Genome Analysis*, 1:543-559 (1997)).

IN THE CLAIMS

Please cancel non-elected claims 8-19 without prejudice to or disclaimer of the subject matter contained therein.

Please amend the claims as follows:

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1. (Amended) A substantially purified nucleic acid molecule, said nucleic acid molecule capable of specifically hybridizing under conditions of 6.0 X sodium chloride/sodium citrate (SSC) at about 45°C, followed by a wash of 2.0 X SSC at 50°C to a second nucleic acid molecule having a nucleic acid sequence of SEQ ID NO: 1 or a complement thereof.